Entrez   PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   Boo

Search Nucleotide ▾ for [   ] Go Clear

Limits   Preview/Index   History   Clipboard   Details

Display | default ▾ Show: 20 ▾ Send to File ▾ Get Subsequence Fea

☐ 1: X96983. Reports B.subtilis chromo...[gi:1239975]   Links

```
LOCUS       BS75DGREG                21808 bp    DNA     linear   BCT 05-JUL-1999
DEFINITION  B.subtilis chromosomal DNA (region 75 degrees: cspB upstream of
            glpPFKD operon).
ACCESSION   X96983
VERSION     X96983.1  GI:1239975
KEYWORDS    cold shock protein; cspB gene; yhcA gene; yhcB gene; yhcC gene;
            yhcD gene; yhcE gene; yhcF gene; yhcG gene; yhcH gene; yhcI gene;
            yhcJ gene; yhcK gene; yhcL gene; yhcM gene; yhcN gene; yhcO gene;
            yhcP gene; yhcQ gene; yhcR gene; yhcS gene; yhcT gene; yhcU gene;
            yhcV gene; yhcW gene; yhcX gene; yhxA gene.
SOURCE      Bacillus subtilis
  ORGANISM  Bacillus subtilis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE   1  (bases 4956 to 5615)
  AUTHORS   Willimsky,G., Bang,H., Fischer,G. and Marahiel,M.A.
  TITLE     Characterization of cspB, a Bacillus subtilis inducible cold shock
            gene affecting cell viability at low temperatures
  JOURNAL   J. Bacteriol. 174 (20), 6326-6335 (1992)
  MEDLINE   93015680
   PUBMED   1400185
REFERENCE   2
  AUTHORS   Beijer,L., Nilsson,R.P., Holmberg,C. and Rutberg,L.
  TITLE     The glpP and glpF genes of the glycerol regulon in Bacillus
            subtilis
  JOURNAL   J. Gen. Microbiol. 139 (Pt 2), 349-359 (1993)
  MEDLINE   93171878
   PUBMED   8436953
REFERENCE   3  (bases 1 to 21808)
  AUTHORS   Noback,M.A., Terpstra,P., Holsappel,S., Venema,G. and Bron,S.
  TITLE     A 22 kb DNA sequence in the cspB-glpPFKD region at 75 degrees on
            the Bacillus subtilis chromosome
  JOURNAL   Microbiology (Reading, Engl.) 142 (Pt 11), 3021-3026 (1996)
  MEDLINE   97124185
   PUBMED   8969498
REFERENCE   4  (bases 1 to 21808)
  AUTHORS   Noback,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-1996) Noback M. A., University of Groningen,
            Dept. of Genetics, Kerklaan 30, Haren, 9751 NN The Netherlands
FEATURES             Location/Qualifiers
     source          1..21808
                     /organism="Bacillus subtilis"
                     /mol_type="genomic DNA"
                     /strain="168"
                     /db_xref="taxon:1423"
                     /map="75 degrees, upstream of glpPFKD"
     gene            1..256
                     /gene="yhcA"
     CDS             <1..256
```

```
                           /gene="yhcA"
                           /codon_start=2
                           /transl_table=11
                           /product="hypothetical protein"
                           /protein_id="CAA65684.1"
                           /db_xref="GI:1239976"
                           /db_xref="GOA:P54585"
                           /db_xref="UniProt/Swiss-Prot:P54585"
                           /translation="SNLMVNMNVSYDTAKTYVYSHIYKHASLDSNVMGINDAFMWATL
                           FCVAGLILSIFLRDVRKDKLRKKKKEELSLLPAPKEAKES"
     gene                  join(264..270,279..809)
                           /gene="yhcB"
     RBS                   264..270
                           /gene="yhcB"
     CDS                   279..809
                           /gene="yhcB"
                           /note="similarity to trp repressor-binding protein wrbA
                           from Escherichia coli (Swiss Prot P304849) and to
                           flavodoxin from Clostridium acetobutylicum (Swiss Prot
                           P18855)."
                           /codon_start=1
                           /transl_table=11
                           /product="hypothetical protein"
                           /protein_id="CAA65685.1"
                           /db_xref="GI:1239977"
                           /db_xref="GOA:P54586"
                           /db_xref="UniProt/Swiss-Prot:P54586"
                           /translation="MKIYVVYDSEGEHTKVLAEAIAEGARENDAAEVFIDHVDQADIR
                           KLKDMDAIIWGCPGHFGTISSGLKTWIDRLGYLWAEGELINKVGAVFCTTATTHGGLE
                           MTMHNLITPMFHQGMIVVGLPGNVPENALYGSYYGAGVTCPVDSDELMSEEGIQLGRA
                           LGRRVSQVTGNLTAGQ"
     gene                  join(808..816,822..1196)
                           /gene="yhcC"
     RBS                   808..816
                           /gene="yhcC"
     CDS                   822..1196
                           /gene="yhcC"
                           /codon_start=1
                           /transl_table=11
                           /product="hypothetical protein"
                           /protein_id="CAA65686.1"
                           /db_xref="GI:1239978"
                           /db_xref="GOA:P54587"
                           /db_xref="UniProt/Swiss-Prot:P54587"
                           /translation="MAIIIAIIAAVIVIAALITFNVRNASPGPEKQEATDRIAPPEEE
                           KNEAHYPAEARAAEHTPSVVKNDSPKEKRDTMGDDIYRQALQKFKHSDEVHAEEEVTE
                           ESDKMQDRSYRDALLSMKNKKK"
     gene                  1186..1190
                           /gene="yhcD"
     RBS                   1186..1190
                           /gene="yhcD"
     gene                  1196..1351
                           /gene="yhcD"
     CDS                   1196..1351
                           /gene="yhcD"
                           /codon_start=1
                           /transl_table=11
                           /product="hypothetical protein"
                           /protein_id="CAA65687.1"
                           /db_xref="GI:1239979"
```

```
                         /db_xref="UniProt/Swiss-Prot:P54588"
                         /translation="MKKANPFTHAGLPFLLFPSIMFLSNKSMEYVVFHLDLVYYVTHT
                         PRIFSGR"
terminator               1199..1239
                         /gene="yhcD"
gene                     1343..1348
                         /gene="yhcE"
RBS                      1343..1348
                         /gene="yhcE"
gene                     1356..2117
                         /gene="yhcE"
CDS                      1356..2117
                         /gene="yhcE"
                         /codon_start=1
                         /transl_table=11
                         /product="hypothetical protein"
                         /protein_id="CAA65688.1"
                         /db_xref="GI:1239980"
                         /db_xref="GOA:P54589"
                         /db_xref="UniProt/Swiss-Prot:P54589"
                         /translation="MNSFLGLLKKDIKLSRMWLLVWICGIIFLLGTGHIIASRTKEPL
                         VIFGFFVAVAFFLLFLSPVFVFYHLRKEGKSQLWLYNPNGGLWLFSSKLAASLLYQFV
                         IQLALTAYGIWMYHMLSVKNLLEHQVDITSTVALLNMYGLISSLDMSVTVIVFWTVFH
                         SLRNWRGMRWAAMVLLVAMWLFFDEYIISPLVESQKHFWPVTVYCNFDFHFHNVWRLE
                         LKPIHLSVLGFPIAIVITFLLLIMASKLLDRKVEV"
gene                     2108..2112
                         /gene="yhcF"
RBS                      2108..2112
                         /gene="yhcF"
gene                     2120..2485
                         /gene="yhcF"
CDS                      2120..2485
                         /gene="yhcF"
                         /note="similarity to members of the gntR regulator family
                         like the korA protein from Streptomyces lividans (Swiss
                         Prot P22405) and farR from Escherichia coli (Swiss Prot
                         P13669)."
                         /codon_start=1
                         /transl_table=11
                         /product="hypothetical protein"
                         /protein_id="CAA65689.1"
                         /db_xref="GI:1239981"
                         /db_xref="GOA:P54590"
                         /db_xref="UniProt/Swiss-Prot:P54590"
                         /translation="MDNQFQSSKPIYLQIADQIFYRLVRKELLPGDKLPSVREMAIQT
                         KVNPNTIQRTYSEMERLGIVETRRGQGTFIAEKAEIVDELKDKLTREVLEGFVKQMKE
                         LGLTKEEMLEGIKTFTEGG"
gene                     2473..2481
                         /gene="yhcG"
RBS                      2473..2481
                         /gene="yhcG"
gene                     2487..3185
                         /gene="yhcG"
CDS                      2487..3185
                         /gene="yhcG"
                         /note="similarity to ABC transporters like the sulfate
                         transport protein cysA from Synechococcus (Swiss Prot
                         P14788) and the copper transport protein nosF from
                         Pseudomonas stutzeri (Swiss Prot P19844)."
                         /codon_start=1
```

```
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="CAA65690.1"
                        /db_xref="GI:1239982"
                        /db_xref="GOA:P54591"
                        /db_xref="UniProt/Swiss-Prot:P54591"
                        /translation="MEIKLEHVSKKYGRHTAVNDVSITLSSGRIYGLIGPNGSGKSTT
                        LKMMAGLLFPTSGFVKVDEEQVTREMVRQTAYLTELDMFYPHFTVKDMVNFYQSQFPD
                        FHTEQVYKLLNEMQLNPEKKIKKLSKGNRGRLKIVLALARRADVILLDEPFSGLDPMV
                        RDSIVNSLVSYIDFEQQIVVIATHEIDEIETLLDEVIILANGEKVAQREVEDIREQEG
                        MSVLQWFKSKMEVC"
gene                    join(3187..3195,3202..4119)
                        /gene="yhcH"
RBS                     3187..3195
                        /gene="yhcH"
CDS                     3202..4119
                        /gene="yhcH"
                        /note="similarity to ABC transporters like the copper
                        transport protein nosF from Pseudomonas stutzeri (Swiss
                        Prot P19844) and yhcG (this submission)."
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="CAA65691.1"
                        /db_xref="GI:1239983"
                        /db_xref="GOA:P54592"
                        /db_xref="UniProt/Swiss-Prot:P54592"
                        /translation="MKTVLELKNVTKNIRGRTIIDDLSFTIREGEVFGFLGPNGAGKT
                        TTIRMMVGLMKLSKGDVLICGQSITKEYAKAIKHIGAIVENPELYKFLSGYKNLQQFA
                        RMVKGVTKEKIDEVVELVGLTDRIHDKVKTYSLGMRQRLGLAQCLLHDPKVLILDEPT
                        NGLDPAGIREIRDHLKKLTRERGMAVIVSSHLLSEMELMCDRIAILQKGKLIDIQNVK
                        DENIDENDTYFFQVEQPSEAATVLNQYDLLSKTNGVEIKLAKEEVPAVIELLVMQQIR
                        IYEVKVITKSLEDRFLEMTGETKEEVQHA"
gene                    4097..4105
                        /gene="yhcI"
RBS                     4097..4105
                        /gene="yhcI"
gene                    4112..5053
                        /gene="yhcI"
CDS                     4112..5053
                        /gene="yhcI"
                        /note="similarity to the membrane protein nosY from
                        Pseudomonas stutzeri, involved in copper processing (Swiss
                        Prot P19845)."
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="CAA65692.1"
                        /db_xref="GI:1239984"
                        /db_xref="GOA:P54593"
                        /db_xref="UniProt/Swiss-Prot:P54593"
                        /translation="MLNLIYNEWLKIFSRAGTWVMIGILGLTMVGFAFLANHFSAGES
                        NSHWKQELQAQNAELKKEIKEDPSLKDGYKETITLNDYRIEHNIPSDTGYTVWSYVTD
                        SANFTILTGLFTIIIAAGIVANEFNWGTIKLLMIRPLSRFQILMSKYITVLLFGLLLL
                        LILFIGSTLLGLIFFGTGGETAANIHLIYKDGHVIEQNMMGHLATTYLSESVSALMVA
                        TMAFMLSAVFRNSSLAVGFSIFLLVAGTTATAFIAAKFDWAKYILFANVDLTQYVDGT
                        PLIKGMTMTFSLVMLAIYFIIFLLLAFGIFMKRDIAN"
conflict                4969..4970
                        /gene="yhcI"
                        /citation=[1]
```

```
                     /replace="t"
     conflict        4973
                     /gene="yhcI"
                     /citation=[1]
                     /replace="g"
     conflict        4990
                     /gene="yhcI"
                     /citation=[1]
                     /replace="g"
     terminator      5055..5091
     terminator      complement(5100..5129)
     conflict        5143..5144
                     /citation=[1]
                     /replace="cg"
     gene            complement(5145..5361)
                     /gene="cspB"
     CDS             complement(5145..5348)
                     /gene="cspB"
                     /note="see EMBL X59715"
                     /citation=[1]
                     /codon_start=1
                     /transl_table=11
                     /product="cold shock protein"
                     /protein_id="CAA65693.1"
                     /db_xref="GI:1239985"
                     /db_xref="GOA:P32081"
                     /db_xref="UniProt/Swiss-Prot:P32081"
                     /translation="MLEGKVKWFNSEKGFGFIEVEGQDDVFVHFSAIQGEGFKTLEEG
                     QAVSFEIVEGNRGPQAANVTKEA"
     RBS             complement(5356..5361)
                     /gene="cspB"
     conflict        5478
                     /citation=[1]
                     /replace="c"
     conflict        5523
                     /citation=[1]
                     /replace="cc"
     gene            5769..6575
                     /gene="yhcJ"
     RBS             5769..5773
                     /gene="yhcJ"
     CDS             5784..6575
                     /gene="yhcJ"
                     /note="similarity to lipoprotein-28 precursor nlpA from
                     Escherichia coli (Swiss Prot P04846)."
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="CAA65694.1"
                     /db_xref="GI:1239986"
                     /db_xref="GOA:P54594"
                     /db_xref="UniProt/Swiss-Prot:P54594"
                     /translation="MKKWLICSFVLVLLVSFTACSPSAEHESIKIGIAESDGAIWNYI
                     AQKAEEAGLDIQLIPFSDYAESDIALANKEIDANAFQTISYFQSFTEKYKLNLAPLGT
                     TYITPMGIYSKRYERIRDISRGAVVSVPDKAFDFGRALTVLQEAGLLTLKNGFNGTGS
                     VDMIKDNPRHLKLKAVRQQDAVSGADVFVMKPSEAKKAGLNPKKHTLKSGGLMSEEEM
                     NLIVVRAEDQDREALQTILELYQADDTAAFIEKEYQGDLVRLFCL"
     terminator      6593..6624
     gene            complement(6616..7709)
                     /gene="yhcK"
```

```
CDS            complement(6616..7695)
               /gene="yhcK"
               /note="similarity to hypothetical proteins from
               Streptomyces ambofaciens (Swiss Prot P36892) and ORF3 from
               Vibrio anguillarum (Genbank U17054)."
               /codon_start=1
               /transl_table=11
               /product="hypothetical protein"
               /protein_id="CAA65695.1"
               /db_xref="GI:1239987"
               /db_xref="GOA:P54595"
               /db_xref="UniProt/Swiss-Prot:P54595"
               /translation="MLKELFVNLTILITFNYLFTHLFKERLVHKKDSISFQAVKGLAC
               GLLGVILMVFGFTYQHSIIDLRNIPIMIAALYGGWVSTATALAMITAGRLLITMNTSA
               LYSVIIICIAAIPSLIVSRRKKVQLKHAFYLLIITNSLISFSYFLIDLHSYELHLYF
               WIISIAGGMLSLYIIDHETNAHLLFKQYKFQAHFDFLTGVYNRRKFEETTKALYQQAA
               DTPHFQFALIYMDIDHFKTINDQYGHHEGDQVLKELGLRLKQTIRNTDPAARIGGEEF
               AVLLPNCSLDKAARIAERIRSTVSDAPIVLTNGDELSVTISLGAAHYPNNTEQPGSLP
               ILADQMLYKAKETGRNRVCFSEKKE"
RBS            complement(7705..7709)
               /gene="yhcK"
gene           7849..9259
               /gene="yhcL"
RBS            7849..7857
               /gene="yhcL"
CDS            7868..9259
               /gene="yhcL"
               /note="similarity to the proton/sodium-glutamate symport
               protein gltT from Bacillus caldotenax (Swiss Prot
               P24944)."
               /codon_start=1
               /transl_table=11
               /product="hypothetical protein"
               /protein_id="CAA65696.1"
               /db_xref="GI:1239988"
               /db_xref="GOA:P54596"
               /db_xref="UniProt/Swiss-Prot:P54596"
               /translation="METLLVVLHVFILFLLILGLFVMQKKHVSFSKRVFTALGLGIVF
               GFALQLIYGPTSNIVIQTADWFNIAGGGYVKLLQMVVMPLVFISILGAFTKLKLTKNL
               GKISGLIIGILVATTAVAAAVGIASALSFDLQAIQVDQGSTELSRGQELQQKSEDMTA
               KTLPQQIVELLPGNPFLDFTGARPTSTIAVVIFAAFLGVAFLGVKHKQPEQAETFKKL
               VDAVYAIVMRVVTLILRLTPYGVLAIMTKTIATSDLDSILKLGMFVIASYAALITMFI
               IHLLLLTFSGLNPVIYLKKAVPVLVFAFTSRSSAGALPLNIKTQRSMGVPEGIANFAG
               SFGLSIGQNGCAGIYPAMLAMMIAPTVGQNPFDPVFIITVIAVVAISSFGVAGVGGGA
               TFAALLVLSSLNMPVALAGLLISIEPLIDMGRTALNVSGSMTSGLITSKVTKEIDQGA
               FHDQSRVIEAEEA"
terminator     9266..9297
gene           complement(9299..9765)
               /gene="yhcM"
CDS            complement(9299..9754)
               /gene="yhcM"
               /note="glutamine-rich protein."
               /codon_start=1
               /transl_table=11
               /product="hypothetical protein"
               /protein_id="CAA65697.1"
               /db_xref="GI:1239989"
               /db_xref="UniProt/Swiss-Prot:P54597"
               /translation="MLFNQRRGISPAALIIGSTMLITALSPQIRQRISGFITGQMNRR
               NSENNTFDASNVGNMVKQAFSGSSGSSGDNQDRSQHQSQRQNGRQHQHAGQQQPQHQH
```

```
                        TQSQTRQTETAAKKRQPHYAEPIHFEQNAMNVMDDNTMMEMLEDLEPGR".
RBS                     complement(9757..9765)
                        /gene="yhcM"
gene                    9890..10473
                        /gene="yhcN"
RBS                     9890..9897
                        /gene="yhcN"
CDS                     9904..10473
                        /gene="yhcN"
                        /note="asparagine-rich protein. Similarity to CS3 pili
                        synthesis protein from Escherichia coli (Swiss Prot
                        P15487)."
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="CAA65698.1"
                        /db_xref="GI:1239990"
                        /db_xref="GOA:P54598"
                        /db_xref="UniProt/Swiss-Prot:P54598"
                        /translation="MFGKKQVLASVLLIPLLMTGCGVADQGEGRRDNNDVRNVNYRNP
                        ANDDMRNVNNRDNVDNNVNDNANNNRVNDDNNNDRKLEVADEAADKVTDLKEVKHADI
                        IVAGNQAYVAVVLTNGNKGAVENNLKKKIAKKVRSTDKNIDNVYVSANPDFVERMQGY
                        GKRIQNGDPIAGLFDEFTQTVQRVFPNAE"
terminator              10472..10510
gene                    join(10641..10644,10653..10952)
                        /gene="yhcO"
RBS                     10641..10644
                        /gene="yhcO"
CDS                     10653..10952
                        /gene="yhcO"
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="CAA65699.1"
                        /db_xref="GI:1239991"
                        /db_xref="UniProt/Swiss-Prot:P54599"
                        /translation="MLAVSSAIVSSAMYILSFPGQASGITKEQVTKHMKKESFKQADI
                        YYTSKEKSLLPLTKETLEYAVSINQIMIGYSNQKPIDIIFFLMKNRWRLTPVYWM"
RBS                     10924..10928
                        /gene="yhcO"
gene                    10943..11560
                        /gene="yhcP"
CDS                     10943..11560
                        /gene="yhcP"
                        /codon_start=1
                        /transl_table=11
                        /product="hypothetical protein"
                        /protein_id="CAA65700.1"
                        /db_xref="GI:1239992"
                        /db_xref="UniProt/Swiss-Prot:P54600"
                        /translation="MDVVGFYSEREQLIGLLPEEKKKLLEGDEVAVYLYQRLLIHEYS
                        HHAFHQKLKELETDPDEFPLWFHEGLSEWIANYELLIDPITFSVVPFDRLQTDRDWQE
                        ARAEYDTDVYLQSFYMIDELTDKYGKDIISEMIKETAKKGDFEKGFKSATKESLDQFE
                        KDFKKKFEKNSAALDSIYPMPLLLVKSLLTHSALCRRHLSLGRGE"
gene                    complement(join(11492..12145,12153..12160))
                        /gene="yhcQ"
CDS                     complement(11492..12145)
                        /gene="yhcQ"
                        /note="similarity to spore coat protein F (cotF) from
                        Bacillus subtilis (Swiss Prot P23261)."
```

```
                              /codon_start=1
                              /transl_table=11
                              /product="hypothetical protein"
                              /protein_id="CAA65701.1"
                              /db_xref="GI:1239993"
                              /db_xref="UniProt/Swiss-Prot:P54601"
                              /translation="MDQFNQQQQSQMNKGIPGKPHKNHGGHEMFDMHEVLSGTLTVLD
                              QFMMLRQFCKDQELLNILDRQHQFITSQYNITAECFKTGSEPSQKTATYMMKEDNQTV
                              YGMQPSQPKKPVQSMNDIDDSIISRQMLCAIKAQASMLTMASLEMTNPAVRRVLSAQI
                              QEYVEMAFEIFLYQNKHGYYQVPQLDAQDMEQLRNSFAPAQGQMPPTQGGMGQQGLH"
```

RBS	complement(12153..12160)
	/gene="yhcQ"
gene	join(12217..12222,12228..15881)
	/gene="yhcR"
RBS	12217..12222
	/gene="yhcR"
CDS	12228..15881

```
                              /gene="yhcR"
                              /note="similarity (C-terminal half) to UDP-sugar hydrolase
                              precursor (ushA) from Escherichia coli (Swiss Prot
                              P07024)."
                              /codon_start=1
                              /transl_table=11
                              /product="hypothetical protein"
                              /protein_id="CAA65702.1"
                              /db_xref="GI:1239994"
                              /db_xref="GOA:P54602"
                              /db_xref="UniProt/Swiss-Prot:P54602"
                              /translation="MLSVEMISRQNRCHYVYKGGNMMRRILHIVLITALMFLNVMYTF
                              EAVKAAEPQQPISIEKAIQQKEGQALVEGYAVGQAVSPQHYKLTSPFSNDYNVALADR
                              KNKTSPEHILPVQIPSAFRSQFGLQTNPLLLGKKITVQGKLENYFNTTGLKNVQSMNV
                              TDDTKTPPAEQQVTINEARGRLNEEVTIKGIITADQNAIGGGKLSTFLQDETGGINIY
                              SPSPEQFPELKEGMDVTVTGKITSYQGLKEIVPNSSGIKINQSNQSLPAPKHLTINEL
                              INGSLGDQYEGRLVKLTAFVSSIPSSPAGGGYNVTMIDDDHHAMTLRVMNETGVINEL
                              DEGKWYEFTGVLSRYQTFQLLPRKSADLKLLEEQPAPPSAEGEYEGIVDRVVDGDTIH
                              LKSPVLGTTKIRFVNVDAPETYHTPKNDADENQLRFGKKASDYLKTVLSPGDKITVKV
                              GSEAKDSYGRLLGQVITESGSNVNLELVKNGYAPTYFIWPVDNEEDYQQFQAAVAAAK
                              KDQKGIWNENDPLMEMPFEFRAREQGKGLTRYVGDSSNKTYVQPADWKKIAVENRIFF
                              ASASEAESAGYKKRQTAPQEHVPLRILSMNDLHGKIDQQYELDLDGNGTVDGTFGRMD
                              YAAAYLKEKKAEKKNSLIVHAGDMIGGSSPVSSLLQDEPTVELMEDIGFDVGTVGNHE
                              FDEGTDELLRILNGGDHPKGTSGYDGQNFPLVCANCKMKSTGEPFLPAYDIINVEGVP
                              VAFIGVVTQSAAGMVMPEGIKNIEFTDEATAVNKAAEELKKKGVKAIAVLAHMSAEQN
                              GNAITGESADLANKTDSEIDVIFAAHNHQVVNGEVNGKLIVQAFEYGKAIGVVDVEID
                              KTTKDIVKKSAEIVYVDQSKIEPDVSASAILKKYETIAEPIISEVVGEAAVDMEGGYS
                              NDGDTPLGNLIADGMRAAMKTDFALMNGGGIREALKKGPITWGDLYNIQPFGNVLTKL
                              EIKGKDLREIINAQISPVFGPDYSISGFTYTWDKETGKAVDMKMADGTEIQPDATYTL
                              TVNNFMATATGAKYQPIGLLGKNPVTGPEDLEATVEYVKSFDEPIAYTKEGRIKLAEA
                              SDIEDPVTEDPITEEPGDDPGTEDPIKEDPRPGEDLPDIKETPGTAPVHQLPPSAISR
                              FNEIPINNTKTADTANSISTLPLQTETAESGSDHQLPDTSAGYYNFMVIGAAVTLSGT
                              YLYVRRKRSASRT"
```

gene	15860..15865
	/gene="yhcS"
RBS	15860..15865
	/gene="yhcS"
gene	15878..16474
	/gene="yhcS"
CDS	15878..16474
	/gene="yhcS"

```
                              /codon_start=1
                              /transl_table=11
```

```
                              /product="hypothetical protein"
                              /protein_id="CAA65703.1"
                              /db_xref="GI:1239995"
                              /db_xref="GOA:P54603"
                              /db_xref="UniProt/Swiss-Prot:P54603"
                              /translation="MKKVIPLFIIAAGLVIAGYGGFKLIDTNTKTEQTLKEAKLAAKK
                              PQEASGTKNSTDQAKNKASFKPETGQASGILEIPKINAELPIVEGTDADDLEKGVGHY
                              KDSYYPDENGQIVLSGHRDTVFRRTGELEKGDQLRLLLSYGEFTYEIVKTKIVDKDDT
                              SIITLQHEKEELILTTCYPFSYVGNAPKRYIIYGKRVT"
    terminator                16473..16501
    gene                      complement(16504..17427)
                              /gene="yhcT"
    CDS                       complement(16504..17412)
                              /gene="yhcT"
                              /note="Similarity to DRAP deaminase from Saccharomyces
                              cerevisiae (PIR S50972) and to a family of hypothetical
                              proteins like yceC from Escherichia coli (Swiss Prot
                              P23851)."
                              /codon_start=1
                              /transl_table=11
                              /product="hypothetical protein"
                              /protein_id="CAA65704.1"
                              /db_xref="GI:1239996"
                              /db_xref="GOA:P54604"
                              /db_xref="UniProt/Swiss-Prot:P54604"
                              /translation="MNQKGRGLEILINEKQDGQWLFSVLKTALKASKPVIQDWMSHQQ
                              IKVNHESVLNNMIVKKGDRVFIDLQESEASSVIPEYGELDILFEDNHMLIINKPAGIA
                              THPNEDGQTGTLANLIAYHYQINGETCKVRHVHRLDQDTSGAIVFAKHRLAHAILDQQ
                              LEKKTLKRTYTAIAEGKLRTKKGTINPPIGRDRSHPTRRRVSPGGQTAVTHFKVMASN
                              AKERLSLVELELETGRTHQIRVHLASLGHPLTGDSLYGGGSKLLNRQALHANKVQAVH
                              PITDELIVAEAPFPADMKNLCRTYFS"
    RBS                       complement(17422..17427)
                              /gene="yhcT"
    gene                      17513..17918
                              /gene="yhcU"
    RBS                       17513..17516
                              /gene="yhcU"
    CDS                       17523..17918
                              /gene="yhcU"
                              /codon_start=1
                              /transl_table=11
                              /product="hypothetical protein"
                              /protein_id="CAA65705.1"
                              /db_xref="GI:1239997"
                              /db_xref="UniProt/Swiss-Prot:P54605"
                              /translation="MARKVIDVRIVNAATAEQESFIKELSMELIHDVFPLYFSELDIQ
                              RLKKKGVLSLNNHYYQGTLKEAFQIMACLQMIHIILTKPSPHSDLSDQAIFEKNSKML
                              NDFGIYFPFAFSDFQKKTNKAFFGQRRLI"
    gene                      18039..18477
                              /gene="yhcV"
    RBS                       18039..18045
                              /gene="yhcV"
    CDS                       18055..18477
                              /gene="yhcV"
                              /note="similarity to IMP dehydrogenase (guaB or gnaB) from
                              Bacillus subtilis (Swiss Prot P21879) and to acuB (acetoin
                              utilization) from Bacillus subtilis (Swiss Prot P39066)."
                              /codon_start=1
                              /transl_table=11
                              /product="hypothetical protein"
```

```
                          /protein_id="CAA65706.1"
                          /db_xref="GI:1239998"
                          /db_xref="UniProt/Swiss-Prot:P54606"
                          /translation="MSSVKDTMTTQVATVSPNQTIQEAASLMKQHNVGAIPVVEQGVL
                         KGMLTDRDIALRTTAQGRDGQTPVSEVMSTELVSGNPNMSLEDASQLMAQHQIRRLPI
                         VDQNNLVGIVALGDLAVNQMSNESAGSALTNISHQNIH"
   terminator            18479..18511
   gene                  join(18589..18594,18604..19266)
                          /gene="yhcW"
   RBS                   18589..18594
                          /gene="yhcW"
   CDS                   18604..19266
                          /gene="yhcW"
                          /note="similarity to phosphoglycolate phosphatase from
                         Alcaligenes eutrophus (Swiss Prot P40852)."
                          /codon_start=1
                          /transl_table=11
                          /product="hypothetical protein"
                          /protein_id="CAA65707.1"
                          /db_xref="GI:1239999"
                          /db_xref="GOA:P54607"
                          /db_xref="UniProt/Swiss-Prot:P54607"
                          /translation="MIKALIFDFDGLILDTETHEYEVLQEIFEEHGSVLPLSVWGKVI
                         GTAAGFRPFEYLEEQIGKKLNHEELTQLRRERFAKRMESEKARPGVEAYLNAAKDLGL
                         KIGLASSSDYKWVSGHLKQIGLFDDFEVIQTADDVEEVKPNPELYLLAAKNLGVSPAE
                         CLAFEDSVNGSIAAKRAGMKCVIVPNKVTGTLMFEDYDHRLESMAEMELALLLDHLNS
                         QN"
   gene                  join(19265..19273,19282..20823)
                          /gene="yhcX"
   RBS                   19265..19273
                          /gene="yhcX"
   CDS                   19282..20823
                          /gene="yhcX"
                          /note="similarity to nitrilase 2 from Arabidopsis thaliana
                         (Swiss Prot P32962) and to a hypothetical protein from
                         Saccharamyces cerevisiae (PIR S51459)."
                          /codon_start=1
                          /transl_table=11
                          /product="hypothetical protein"
                          /protein_id="CAA65708.1"
                          /db_xref="GI:1240000"
                          /db_xref="GOA:P54608"
                          /db_xref="UniProt/Swiss-Prot:P54608"
                          /translation="MSEKLDLTRFEKKMVIRNIEEKDIDKIIDLQKDCFPGMEPWKRE
                         HLISHLEHFPEGQFCAEFEGEIIGSCSSLLINFDEYDDRHTWQDITDDGYITNHNPDG
                         LNMYGIEVMVHPKYRRMKIGHRLYEARKDLARRLSLKSIIIGGRIPNYHKYAEEMTAR
                         EYVEQVTRHQIYDPVLSFQLMNGFTLMRINPNYLPDDTASIKYATLMEWNNVDYLPQQ
                         TKRYYKSAFPVRICVIQYEMKKIYSFEEFANQVEYYVDVASDARSDFAVFPEIFTTQL
                         MSFLEERSPSLAVQRITEYTEDYISLFTDLAVKYNVNIIGGSHFVEEEGKIYNIAYLF
                         RRDGTIEKQYKLHITPNERKWWGISAGDQVRVFDTDCGKIAIQICYDIEFPELARIAA
                         DKGAKIIFTPFCTEDRQGYLRVRYCSQARAVENQIYTVISGTVGNLPQTENMDIQYAQ
                         SGIFAPSDFEFARDGIVGETNPNIEMVVIGDVDLEILRRQRQNGTVRQLKDRRRDIYH
                         IQYKK"
   terminator            20815..20858
   gene                  21227..21808
                          /gene="yhxA"
   RBS                   21227..21232
                          /gene="yhxA"
   CDS                   21243..>21808
                          /gene="yhxA"
```

```
                    /note="This is the N-terminal fragment of a hypothetical
                    protein from which the C-terminal sequence has been
                    published (ORF1 in [3] and YHXA_BACSU in Swiss Prot :
                    P33189). Unpublished sequence from the authors in [3]
                    contains the complete sequence of yhxA. Similarity to DAPA
                    aminotransferase (bioA) from Bacillus sphaericus (Swiss
                    Prot P22805)."
                    /citation=[2]
                    /codon_start=1
                    /transl_table=11
                    /product="hypothetical protein"
                    /protein_id="CAA65709.1"
                    /db_xref="GI:1240001"
                    /db_xref="GOA:P33189"
                    /db_xref="UniProt/Swiss-Prot:P33189"
                    /translation="MEMMGMENIQQNQGLKQKDEQFVWHAMKGAHQADSLIAQKAEGA
                    WVTDTDGRRYLDAMSGLWCVNIGYGRKELAEAAYEQLKELPYYPLTQSHAPAIQLAEK
                    LNEWLGGDYVIFFSNSGSEANETAFKIARQYHLQNGDHSRYKFISRYRAYHGNTLGAL
                    SATGQAQRKYKYEPLSQGFLHAAPPDIYR"
     ORIGIN
        1 ttcgaattta atggtgaata tgaatgtgtc ttatgatacg gcgaaaacat atgtgtactc
       61 acatatttat aaacacgcat cactcgattc caatgtcatg gggataaatg atgcctttat
      121 gtgggcaacc ttattctgtg tagcaggttt gattttaagt atcttcctgc gtgacgtcag
      181 aaaagataaa ttgcgtaaga agaaaaaaga ggagctttca ttacttcctg ctccaaaaga
      241 agctaaggaa tcttaatctg tacagggagg tttcctgaat gaaaatttat gtagtgtatg
      301 atagtgaagg cgaacatact aaagtgcttg cagaagcgat tgctgaaggc gcgagagaaa
      361 acgacgcggc tgaagtgttc atcgaccatg tagatcaggc tgatatccgc aagcttaaag
      421 atatggatgc gattatttgg ggatgcccag ggcatttcgg aacaatcagc tccggtctta
      481 aaacttggat cgacagactt ggctacttgt gggctgaagg cgagctgatc aacaaagtcg
      541 gtgctgtctt ctgcacaacg gcaacaacac acggcggctt ggaaatgaca atgcacaatt
      601 taatcacgcc gatgttccac caaggcatga ttgttgtcgg actgcctggc aacgtgcctg
      661 aaaacgcact ttatggctct tattacggag caggtgtcac ttgtccggta gacagtgatg
      721 agttaatgtc tgaggaaggt attcagcttg acgcgcgtt gggaagacgt gtcagccaag
      781 tcacaggaaa cctaacagca ggacagtaag gagaggttga aatggccatt attatagcaa
      841 taattgctgc tgtcattgtc attgcggccc ttattacatt taacgtccgc aacgcctcac
      901 ctggacctga gaagcaagaa gcaaccgata gaatcgcacc tccagaagag gaaaaaaacg
      961 aagcgcatta ccctgctgaa gcaagggctg ccgagcatac gccatccgtt gtcaaaaacg
     1021 attctccaaa agagaagcgt gacacaatgg gtgatgatat ttacaggcag gcgctgcaaa
     1081 agtttaagca ttctgatgaa gttcatgcag aagaagaggt cactgaggaa agtgacaaaa
     1141 tgcaggaccg cagctatcgt gatgcgctgc tctctatgaa aaataagaaa aagtaatgaa
     1201 aaaggcaaat ccgtttactc atgcgggttt gcctttttg ctgtttccat caattatgtt
     1261 tttatcaaat aaatccatgg aatatgttgt attccacctt gatctagtgt actatgttac
     1321 tcatacaccg aggatttttt ccgggaggta aagacatgaa ttctttttta ggtttattaa
     1381 agaaagatat caagctttca agaatgtggc tgctagtatg gatatgcgga atcattttct
     1441 tattgggaac aggccatatt atagcttctc gcacgaaaga acctctagtc attttggtt
     1501 tttttgttgc agttgctttt tttctgcttt tcttatctcc tgtttttgtt ttttatcacc
     1561 ttcgcaagga agggaaatca cagctttggc tgtacaatcc aaatggcggc ttatggctgt
     1621 tttcttctaa attggcagca tctttgctct atcaatttgt gattcagttg cattaacag
     1681 cctatggcat atggatgtat catatgctct ctgtaaaaaa tctgctggag catcaagttg
     1741 atataacgag tacagtggct ttgctgaata tgtatgggct tatttcttcg ttagatatgt
     1801 cagtaacagt cattgtgttt tggactgttt ttcactctct cagaaattgg cgcggaatgc
     1861 ggtgggctgc gatggttctg ttggtcgcaa tgtggttatt cttcgatgaa tacatcataa
     1921 gccctttggt tgaatctcaa aagcatttct ggcctgtaac agtctattgc aattttgatt
     1981 tccacttcca caatgtttgg agattggaac taaaacctat ccatctgtct gtgctaggt
     2041 ttcctattgc tatagtcatc acattcttgc tgctcatcat ggcttcaaaa ctgcttgatc
     2101 gtaaagtaga ggtgtaaata tggacaatca attccaatcc tcgaaaccga tttatctgca
     2161 gatcgctgat cagatctttt ataggctggt caggaaggag ctgctcccag agacaagct
     2221 tccttcagta agagaaatgg cgattcaaac taaagtaaat cccaatacaa ttcaaagaac
     2281 ttacagtgag atggaaaggc tgggtattgt ggagacaaga agaggtcaag ggacgtttat
     2341 tgcggaaaaa gcagaaatcg tagacgagct gaaagacaag ctgacacgag aggtgctgga
```

```
2401 aggctttgtc aagcaaatga aagagctggg gctaacgaaa gaagaaatgt tagaggggat
2461 taaaacattc acagagggag gctaaaatgg aaatcaagct agaacatgta tcaaaaaaat
2521 acggccgcca tacggccgtc aatgatgtgt caatcaccct atcatccgga cggatttatg
2581 gcctgattgg accgaacggc agcggcaagt caacgaccct gaaaatgatg gctggccttc
2641 tgtttccgac ttcaggattt gtaaaagttg atgaagagca ggttacgaga gaaatggtgc
2701 gtcaaacggc ttatcttact gagcttgata tgttttatcc gcatttcact gttaaagata
2761 tggtgaattt ttatcagtcg cagtttcctg attttcatac agaacaggtt tataagctat
2821 tgaatgagat gcagctgaat ccggaaaaaa agatcaaaaa gctatcaaaa ggaaatcggg
2881 gcaggctgaa aatcgttctt gctttagcga gacgggcaga cgtcatcttg cttgatgaac
2941 ctttttccgg gcttgatccg atggtcaggg attccatcgt aaacagcctt gtgtcgtaca
3001 ttgattttga gcagcagatt gtcgtgatcg cgacacatga aattgatgaa attgagactt
3061 tgttagatga agtaatcatc ctcgccaatg gagaaaaagt tgcgcagcgt gaagtagaag
3121 atattcgtga acaggaaggc atgtctgttt tgcaatggtt taaatcaaaa atggaagttt
3181 gctagaaaga ggaggaatat gatgaaaaca gtgttggaat tgaaaaacgt gactaaaaac
3241 atcagaggcc gaacgatcat tgatgatctc agttttacga ttcgtgaagg cgaggtattc
3301 ggttttttag gaccaaacgg agcggggaaa acgacaacca tccggatgat ggtgggggtta
3361 atgaagctgt cgaaaggtga tgtcctcatt tgcggccaat caattacgaa agaatatgcc
3421 aaggcgatta agcatatcgg agcgatcgtt gagaatcccg agctgtataa atttttgagc
3481 ggatataaaa atctccagca attcgcaagg atggtcaagg gtgtcacgaa ggaaaaaatt
3541 gatgaagttg ttgaactggt cggtttaaca gacagaatcc acgacaaggt gaaaacatat
3601 tctctgggga tgagacagcg tcttggcttg gcacaatgcc ttctgcacga tccgaaagtg
3661 ctgatttttgg atgaaccgac aaacggcctt gatccggcgg ggatcagaga aatcagagat
3721 catttaaaga agctgacccg agaaagagga atggctgtca tcgtttcaag ccacctgctg
3781 tcagaaatgg aactgatgtg tgatcgaatt gcgattctgc aaaaaggaaa gctgatcgat
3841 attcaaaatg taaaagatga aaacattgat gagaatgata catatttctt ccaggttgag
3901 cagccgagtg aagccgctac tgtttttaaat cagtacgatt tgctgagtaa gacaaatggt
3961 gtagaaatca aactggctaa agaggaagtc cctgcggtta ttgaattgct ggtgatgcag
4021 caaatccgta tttatgaggt caaggtcata acaaaatcat tagaggaccg tttcttagaa
4081 atgacaggtg aaacaaaaga ggaggttcag catgcttaat ttgatttata atgagtggct
4141 caaaattttc agccgtgccg gaacatgggt gatgatcgga attctggggc tgacaatggt
4201 tggatttgca tttttggcga tcattttttc tgccggtgaa tcaaattccc attggaaaca
4261 agagcttcaa gcacaaaacg ccgaattaaa gaaagaaatc aaagaagatc cttcactgaa
4321 agatgggtat aaagaaacaa tcacactcaa tgactatcgc atcgagcata atatccctag
4381 tgacacgggc tatacggtat ggtcttatgt aacggattca gcaaacttta ccatccttac
4441 cggtctgttt actattatca tcgcggccgg aattgtcgcg aacgaattta attggggaac
4501 gattaagcta ttaatgattc ggccgctcag tcgttttcaa attttgatgt ccaaatatat
4561 tacagttctc ctgtttgggc tcctgttgct gttgatttta tttatcggtt ctactttatt
4621 agggttgatc ttcttcggaa cgggtggtga aaccgccgcg aatattcatt taatctataa
4681 ggatggccat gtcattgagc aaaacatgat ggggcatttg gctacaacgt atctttctga
4741 atccgtctcg gctttaatgg tggcgacgat ggcgtttatg ctgtctgcgg tattcagaaa
4801 cagctctctt gcggttggtt tttccatctt cttgttggtt gccggtacga ctgcaactgc
4861 atttattgca gcgaaatttg actgggcaaa gtatatattg tttgctaatg tcgacttgac
4921 tcagtatgtg gatggcacac cgttaataaa agggatgact atgacgtttt ctctcgtcat
4981 gctggcgatc tactttatca tcttcctgtt gcttgctttc ggaatcttca tgaagcggga
5041 tattgcaaac taataaaaaa agctgttttg cttatgcaaa acagcttttt tgtcaaaata
5101 aaaactgcag gtttgcacct gcagtttttc atatcaattt atgcttacgc ttctttagta
5161 acgttagcag cttgtggtcc gcggtttcct tcaacgattt caaaagaaac agcttggcct
5221 tcttctaaag ttttgaagcc ttcgccttga atagcagaga aatgaacgaa tacatcgtct
5281 tgaccttcta cttcgatgaa tccgaaacct ttttcagagt tgaaccattt tactttacct
5341 tctaacatga aatttcctcc taaagcgatc ataacgctta aattcactat tcttgctctt
5401 aacaaacttt caagacgaaa actcttacaa aactttcttc ttaaagatag ttcgaacaaa
5461 aataattacc tttactctac cagtaatctt cagaaaaaac aactgcttat tgaaattttt
5521 ttcggaaaat accatatttta tttttcaatt tgatatttat ttacggaaat tcatctgttt
5581 tctcgatatg tgatcatacg tttgccttag tattccttca ttttgggaag ataagtaata
5641 ggaattgaca accttattgg atatgagtaa ggtaaaagtt aatcaatatt acaaatgaca
5701 acgtttatca actaagagag cgtatgattt ttatgtctga tattgcttgc atgctctaat
5761 acatagatag gagtatggtc acaatgaaaa agtggcttat atgcagtttc gtccttgttc
5821 ttctcgtttc atttactgca tgttcaccgt ctgcagaaca tgaatcgata aaaatcggga
5881 ttgctgagtc tgacggggca atatggaact atattgctca aaaggctgaa gaggcagggc
5941 tggatattca gctgatccct ttttctgatt atgcggagtc tgatatcgca cttgctaaca
```

```
6001 aagaaattga tgccaacgcc tttcaaacca tttcatattt tcagtcgttc actgaaaaat
6061 acaaacttaa tttggcaccg ctcgggacga catacataac gcccatgggc atttattcaa
6121 aacgatatga acgaatccga gatatatcgc ggggagctgt cgtttctgtt ccggataaag
6181 cgttcgattt tggcagggcg cttacggtgc tccaggaagc gggtttgcta acgctgaaaa
6241 acggatttaa cggaacaggt tcagttgata tgattaaaga taatccgaga cacctgaaat
6301 taaaagctgt ccggcaacag gatgcagtga gcggtgccga cgtgtttgtc atgaaaccat
6361 cagaagcaaa aaaagcgggc ttgaacccga aaaagcatac gctaaagagc ggcggactca
6421 tgtctgagga agagatgaat ttgattgttg tcagagcgga ggatcaagat cgggaagcgc
6481 tgcaaaccat tcttgagctt tatcaagctg atgatacagc ggcatttata gaaaaagaat
6541 atcagggaga tcttgtccgg ctttttctgcc tttgaaacgt ctttcagatt ggaagaatga
6601 attcgaacat tgaattcatt ctttttttttc tgaaaaacac actctgttcc gtcccgtttc
6661 tttcgctttg taaagcattt gatcggcaag aatgggcaag gatcctggct gttccgtatt
6721 attggggtaa tgagcggccc ctagtgatat cgtaactgaa agctcgtcgc cgtttgttaa
6781 tacaatcggt gcatcactta cagtgctcct gatccgttca gcgatccggg ctgctttatc
6841 aagagaacag ttcggcagga gcacggcaaa ttcttcaccg ccgatccgag cggcaggatc
6901 agtatttcgg atggtctgct tcagacgtaa ccctagctct ttgagcacct gatctccttc
6961 atgatggcca tattggtcat tgatggtctt aaaatgatcg atatccatat aaatcagtgc
7021 aaattgaaaa tgcggggtat cggccgcctg ctgatacaga gcttttgtgg tttcttcaaa
7081 ttttcttcgg ttatacacgc ctgttaaaaa gtcaaagtgc gcctgaaact tatattgttt
7141 aaaaagaaga tgtgcatttg tttcatgatc aataatatat aaactgagca tgccgcccgc
7201 tattgatatg atccaaaaat acaaatgaag ttcgtatgaa tgtaaatcta taagaaaata
7261 aaaggaaaag gagatcaagc tatttgtgat tattaaaaga tagaaagcat gttttagttg
7321 aacttttttt cttctagaaa caatgagtga cggaatggca gcgatacaaa tgataataac
7381 cgagtatagt gcagatgtgt tcatcgtaat cagcaagcgg cctgcagtga tcatggccag
7441 ggccgttgcc gttgaaaccc agcctccata aagagcggca atcataatag ggatatttcg
7501 aagatcaata attgaatgct gataggtaaa tccaaaaacc atcagaataa ccccgagcaa
7561 accgcaggcc agtcctttaa cagcttgaaa ggatatgctg tcttttttat gtactagcct
7621 ttctttaaac aggtgggtga agagataatt aaatgtgatt aaaatggtca aatttacaaa
7681 cagttctttc agcaaatatt atcaccctta tataaggtac taaagatgga agggaaagaa
7741 aagaacaaaa aaggcattat ataaggtttt tttacttgaa ttgataagtt aaaataattc
7801 gcacttgacc catcggaatt agtgtaatat agtaaatgag aaaatttgaa gggagagttt
7861 acctgctttg gagactttac tggttgtatt acatgtattt attttatttt tacttatctt
7921 agggctcttt gttatgcaga aaaaacatgt ttccttctct aaacgtgtat ttactgcgct
7981 ggggctgggg attgtattcg gatttgcgct tcagctgatt tacggcccga cttcaaatat
8041 agtcattcaa acagccgact ggtttaatat tgccgggggc ggatatgtca aattgcttca
8101 gatggttgtc atgccgctcg tctttatttc gattctcggc gcctttacaa agctgaagct
8161 gacaaaaaat cttgggaaaa tcagcggttt gattatcggg atttttagtag caacaacagc
```
```
8221 agttgctgca gctgtcggta tcgcgtccgc gctttcattt gatctgcagg cgattcaggt
8281 tgaccaagga agtacagagc tttcacgggg acaggagctt cagcagaaat cagaggatat
8341 gacagcgaaa acgctgccgc agcagattgt tgaactgctg cctggaaacc cgtttttaga
8401 ttttacggga gctagaccga cttcaacgat cgctgtcgtt attttgccg ctttccttgg
8461 agtggcattc ctcggcgtaa aacacaaaca gccggaacag gcagaaacat ttaaaaaact
8521 ggttgatgcc gtttatgcca ttgtcatgcg tgttgtcaca ctcattttga gactgacgcc
8581 ttatggggtg ctggccatca tgacaaaaac aattgcaacg agtgatcttg acagcattct
8641 aaaactgggc atgttcgtga ttgcatcata tgccgcgtta atcactatgt ttatcattca
8701 tttgctgctg ctgacgttca gcggcttgaa tccggtgatt tatttgaaaa aagcggtgcc
8761 tgtacttgta tttgcattta cgtcaaggtc tagcgcaggt gctttaccgc tgaatattaa
8821 aacacagaga agcatgggtg taccggaggg aatcgcaaac tttgccggtt cgttcggtct
8881 ttcgatcggc caaaatggat gtgccggcat ttatcctgcg atgctggcga tgatgattgc
8941 tccgactgtc ggccaaaatc catttgaccc ggtgtttatt atcactgtta tcgcagtcgt
9001 tgccatcagc tccttcgggg ttgccggagt cggcggcgga gcgacattcg cggcgcttct
9061 tgttttatca tcattaaaca tgcctgtcgc gctcgccggt ttgttaatct caattgaacc
9121 gttaatcgac atggggcgta ctgctttgaa tgtcagcgga agcatgacat ccggtcttat
9181 tacaagtaag gtcacaaaag aaattgatca aggggcattt catgatcaat ccagagtgat
9241 tgaagctgaa gaagcgtaac atatgaaaac gtgtaatcca agaggattac acgttttttt
9301 aacggccagg ctctaagtcc tccagcattt ccatcatcgt gttgtcgtcc atgacattca
9361 ttgcgttttg ttcaaaatga atgggttcag cataatgcgg ctgtcttttt ttcgcggctg
9421 tctcagtttg cctagtttga gactgtgtat gctgatgctg tggttgctgc tgtccagcgt
9481 gctggtgctg acggccattt tgccgctggc tttgatgctg cgaacggtcc tggttatcac
9541 cgctgcttcc gctgcttccg ctaaatgctt gtttgaccat gtttcctaca ttagaagcat
```

```
 9601 caaacgtgtt attttctgaa tttcgtctgt tcatttgtcc tgtgataaac ccgctgattc
 9661 tttggcggat ctgaggtgat aatgcagtaa taagcatagt tgatcctatg atcaatgctg
 9721 cggggctgat tcctcttcgc tggttgaaca acatgatccc tcctttgcag tgtattcata
 9781 ttttccccct cgttagacaa attaaccgtt atatttcccg ggaaagcatt tcctccagat
 9841 ttgcatgcat aattaaagcc agttagaaaa acctataagt aaagtgataa aggaggaatt
 9901 cacatgtttg gaaaaaaaca agtccttgcg tctgtgcttc ttatcccttt gcttatgact
 9961 ggctgcggtg tagccgacca aggtgagggc agacgtgata ataatgatgt aagaaacgta
10021 aattatcgaa atccggccaa tgacgatatg cggaatgtaa acaatcggga taacgttgac
10081 aacaatgtta atgataatgc caataacaat cgtgtaaatg acgataataa caacgaccga
10141 aaacttgagg ttgctgatga agcagctgat aaagtaacag acctaaaaga agtaaagcat
10201 gccgatatca ttgtggctgg aaatcaagcc tacgttgcag tcgtttttaac caatggaaat
10261 aaaggtgcag tagaaaacaa tctgaagaaa aaaatagcca aaaaggtaag atctactgac
10321 aaaaacattg ataatgttta cgtttcagct aaccctgatt ttgtagagcg tatgcaagga
10381 tatggaaagc gtattcaaaa tggtgaccca atcgccggat tatttgatga atttacacaa
10441 actgtacagc gtgtattccc taacgctgaa taaatgaaag aagccgcaca atttgtgcgg
10501 ctttttcttt gcgttaatga cacactgcga actcaggctg catagagtaa aaataaaaag
10561 gtacaagacg gaccggctca gggagggaga cgtttgcggg atggcatagg aaagcgtgcg
10621 catccgctct attcctgtgc ggagtccttg tgatgctggc tgtaagctca gccatcgtat
10681 caagcgcgat gtatatcctg tcttttccag gtcaggcatc tggaataaca aaagaacaag
10741 tgacgaagca catgaagaaa gagtcattca acaggccga tatttattac acttctaagg
10801 aaaagtcctt actgccattg acgaaagaaa cgcttgaata tgcggtcagt attaatcaga
10861 ttatgattgg atattcgaat caaaagccta ttgacattat tttttttccta atgaaaaaca
10921 gatggaggct tactccggtt tattggatgt agttggtttt tattctgaac gggagcagct
10981 gatcggattg ttgcctgaag agaaaaagaa actgttagaa ggggacgagg tagcggttta
11041 tttgtaccag agattgttga ttcatgaata ctcgcaccat gcgtttcacc agaaattgaa
11101 ggagcttgag acggatcccg atgagtttcc gttatggttt catgaagggt taagcgagtg
11161 gattgcgaac tatgaattgc tcatagatcc gatcacgttt tctgtcgtgc cctttgaccg
11221 tttgcagact gatcgagact ggcaggaagc tagagccgaa tatgacactg atgtctattt
11281 gcaaagcttt tatatgatcg atgagctgac ggacaaatac gggaaagaca ttatttcaga
11341 aatgattaag gaaacggcaa aaaaagggga ctttgaaaaa gggtttaaat cagcaacaaa
11401 ggaaagtctt gatcaatttg aaaaagattt taagaaaaaa tttgaaaaaa acagtgcggc
11461 attggatagt atctatccaa tgcctttgtt attagtgaag tccttgctga cccattccgc
11521 cttgtgtcgg aggcatttgt ccttgggcag gggcgaatga atttcgcagc tgttccatat
11581 cctgcgcatc aagctgagga acctggtaat agccgtgttt gttttggtat aggaaaattt
11641 caaatgccat ttcaacatac tcctgaattt gcgcagacag tacgcgtctt acggccggat
11701 ttgtcatttc cagagaagcc atcgtcagca tagaagcttg tgctttaatc gcgcaaagca
11761 tttgtcggct gatgatgctg tcatcaatat cattcatgga ttgaacaggt tttttaggct
11821 gtgacggctg catgccgtaa acagtctggt tgtcttcctt catcatataa gttgctgttt
11881 tttgtgaagg ttcgcttcct gttttgaagc attctgcagt tatattgtat tgagatgtga
11941 tgaattgatg ttgacgatca aggatgttta gtaattcttg atccttacag aattgtctca
12001 gcatcataaa ctgatcaagc acagtaagtg ttccggaaag cacctcatgc atatcaaaca
12061 tttcatgtcc gccgtggttt ttatgcggtt tgccaggaat acctttgttc atttgggatt
12121 gctgctgctg attgaactga tccaaaccga attcctcctt tttttcaga tcagctgtat
12181 tttgtgtcag tctgccgtgt attatgcaga agcctgaaag gaattatatg ctgtctgtcg
12241 aaatgataag cagacaaaat cgttgtcatt atgtgtataa gggaggaaat atgatgaggc
12301 gtattctgca tattgtgttg atcacggcat taatgttctt aaatgtaatg tacacgttcg
12361 aagctgtaaa ggcagctgaa ccgcaacagc ctatatcgat tgagaaggca atacagcaaa
12421 aagaaggaca ggcacttgtc gaaggatatg cagtcggcca ggctgtttcc ccgcagcatt
12481 ataaactgac aagcccttttt tcaaatgatt ataatgttgc gctggcagac cgtaaaaaca
12541 aaacatcgcc cgaacacatc cttcctgtgc aaatcccctc cgccttcaga agccaatttg
12601 ggctgcaaac caatccgctt cttcttggga aaaagataac ggttcaagga aagcttgaaa
12661 attactttaa cacgacagga cttaaaaacg ttcagtcgat gaacgtaacc gatgacacaa
12721 aaactccgcc ggctgaacag caagtgacca taaatgaagc acggggaagg ctgaatgaag
12781 aagtaacgat aaagggatc attacagctg atcaaaacgc aatcggaggc gggaagctgt
12841 cgacctttttt gcaagatgaa accggaggca ttaacattta ttcgccatcc cctgaacaat
12901 ttcccgaatt aaaagagggt atggatgtca cggtgacagg gaaaatcacg tcttaccagg
12961 ggctgaaaga aatcgttcca aactcatcag gcatcaaaat caaccagtca aatcaatccc
13021 tccccgcccc caaacactta acaatcaatg aacttattaa cggcagccta ggtgatcagt
13081 atgaaggacg ccttgtgaaa ctaaccgctt ttgtttcctc aattccaagt tctcctgccg
13141 gcggcggtta caatgtaaca atgattgatg acgaccatca tgcaatgacg ctccgggtta
```

```
13201 tgaatgaaac aggggtgata aacgagcttg atgagggcaa atggtatgaa tttaccggtg
13261 tgttaagcag ataccaaacc tttcagctgc ttccgcgaaa atcggctgac ctgaagctgc
13321 ttgaagagca gcccgcacct ccgtctgcag agggagaata tgaagggatt gttgaccggg
13381 tagttgacgg cgataccatt catcttaaat ctccggtgct tggaacgaca aaaatccggt
13441 ttgtaaatgt agatgcaccc gaaacatatc acacaccaaa aaatgacgca gatgaaaatc
13501 aattaagatt tggcaaaaaa gcatctgact atctaaaaac ggttctgtcc ccgggtgata
13561 aaattactgt caaggtcggg agtgaagcca aggacagcta tggcagattg ctcggacaag
13621 tcataaccga atcaggttca aacgtgaact tagagcttgt aaaaaacggc tatgctccga
13681 cgtattttat ttggccggtt gacaatgaag aggattatca gcaatttcag gccgcagtag
13741 ccgctgcaaa aaaagatcaa aaaggaattt ggaatgaaaa cgatccctc atggaaatgc
13801 cgtttgaatt cagagccaga gagcaaggga aaggcctgac aagatatgtg ggggactcgt
13861 cgaataaaac atatgtgcag ccagctgact ggaagaagat agctgtggaa aacagaattt
13921 tcttcgcctc agcaagtgaa gcggagagcg cgggatataa aaaaaggcaa acggcacctc
13981 aagaacatgt gccgcttaga attctcagca tgaatgattt gcatggcaaa atcgatcagc
14041 aatatgagct tgatcttgat ggaaatggaa ctgtagacgg cacgtttgga cgcatggatt
14101 atgccgccgc atatttaaaa gaaaaaaagg ctgaaaagaa aaactcgctg attgtgcacg
14161 cgggagatat gatcggcgga agctctccag tttcctctct tcttcaggat gaaccgactg
14221 tagaactgat ggaggacatc ggatttgatg tcggaaccgt gggaaaccac gaatttgatg
14281 aaggcacgga tgaacttctg aggatcttaa atggcggtga tcatccgaaa ggcacaagcg
14341 gatatgatgg acagaacttt ccccttgtat gtgccaattg taaaatgaaa tcaactggag
14401 agcccttttt gccggcttac gacatcatta atgtggaggg cgtacccgtt gcttttatcg
14461 gagttgtcac acagtcggca gctggcatgg ttatgcctga aggaataaaa aatatcgagt
14521 ttacagatga agcaacagcg gtgaataagg cggccgaaga gctcaagaaa aaaggcgtga
14581 aggccatcgc ggttctcgca catatgtcag ctgaacaaaa cggcaacgcc attaccggtg
14641 agtctgctga tcttgcaaac aaaacagatt ctgaaattga cgtgattttt gccgcgcata
14701 atcatcaggt tgttaacggt gaagtgaatg gaaaactgat tgttcaagcg tttgaatatg
14761 gaaaagcgat aggtgtcgtt gatgtagaga tcgataaaac gacaaaagac attgtcaaaa
14821 agtccgcgga aatcgtatat gttgatcaaa gtaaaatcga accggatgtc agcgcgtcag
14881 ccattttaaa gaaatacgaa acaattgcgg aaccgattat cagcgaggta gtcggcgaag
14941 ccgctgttga tatggaaggg gggtattcaa atgacggcga tacacctctt ggaaacctga
15001 ttgcggatgg tatgagagct gccatgaaaa cggattttgc ccttatgaat ggcggcggca
15061 tacgtgaagc gctgaagaag ggtccaatta cgtggggaga tctttacaat attcagccgt
15121 ttggaaatgt gttaacgaag cttgagatta aaggaaaaga tttaagagag attatcaatg
15181 cgcaaatctc gccggttttt gggcctgact acagcatcag cgggtttacg tatacgtggg
15241 ataaagaaac cggaaaagca gttgatatga aaatggcaga tggcaccgag atccagcccg
15301 atgccacata tacattgacc gtcaacaact ttatggcgac ggcgacagga gccaaatatc
15361 agccaatcgg actgctggga aaaaatccgg tgacagggcc tgaggatttg gaagcgacag
15421 ttgagtacgt gaagagtttt gatgagccaa ttgcgtatac aaaagaggga agaattaagc
15481 ttgctgaagc cagtgatatt gaagaccctg taacagaaga cccgataacg gaagagcctg
15541 gagatgatcc ggggacggag gatccgatta aagaggatcc aaggccaggt gaagatttgc
15601 ctgatataaa agaaactccg ggaacagcac cggttcatca gcttccgcct tcagccattt
15661 cgagattcaa tgaaatacca atcaacaaca caaaaaccgc tgatactgct aatagcatca
15721 gcacattgcc gttacaaacc gagactgcgg aaagcgggtc tgatcatcag cttccggata
15781 cgtcagcggg ctactataac tttatggtaa tcggtgcggc ggtgacattg tcaggaactt
15841 atctatatgt cagaagaaaa aggagcgcct ccagaacgtg aaaaaagtta ttccactatt
15901 catcattgct gccggcctag tgatcgcagg ctatggaggc tttaaattga tcgatacgaa
15961 tacgaaaacg gaacagacat taaaagaagc aaagctggcg gctaaaaagc cgcaggaagc
16021 ttcggggacg aaaaatagca cagatcaagc aaagaacaaa gcatcattta agcctgagac
16081 cggccaagcg agcggcattt tagaaatacc gaaaatcaat gcagagcttc cgatcgtgga
16141 gggcaccgat gctgatgatt tagaaaaagg tgtcgggcat tacaaggaca gctattatcc
16201 tgatgaaaac ggacaaattg tgctgtcagg gcatcgggat accgtgtttc gccggacggg
16261 agagctggaa aaggggggatc agctccgtct tctcctgtca tatggagaat tcacatatga
16321 aattgtaaaa acaaaaattg tcgataagga tgacacatct attatcacgc tccagcatga
16381 aaaggaagag ctgattctga cgacctgcta tccgtttttca tacgtcggaa atgccccgaa
16441 gcgctatatt atatatggaa aacgagtgac ttaaaaagcc gaggcagtgc ctgcggcttt
16501 tcttcatgaa aaatatgtgc ggcaaaggtt tttcatatca gcagggaaag gggcttcagc
16561 aactatgagc tcgtctgtta tcgggtgaac cgcttgtact ttattggcgt gcagtgcctg
16621 cctgtttagc agcttgctcc cgcctccgta aagcgagtct cctgtcaacg gatggccgag
16681 gctcgccaga tgaacacgga tttggtgtgt tctgcctgtt ccagctctct attcaacgag
16741 cgacagccgt tctttcgcat tgctggccat taccttgaaa tgagtgacgg ctgtttgccc
```

```
16801 gcctggtgaa acccggcgtc ttgtcgggtg tgagcggtct ctgccgatcg gtggactaat
16861 tgtccctttt ttcgtccgta gcttaccttc agcgatagcg gtatacgtac gcttcagcgt
16921 cttttttctct aactgctggt ctaagatggc gtgtgccaaa cgatgcttgg caaaaacgat
16981 agcgccagat gtatcctgat caagacgatg gacgtggcgc accttacatg tttcgccatt
17041 tatctgataa tgatacgcga tcaaattagc cagtgtgccg gtttgcccat cctcattcgg
17101 atgcgtcgcg atgccagcgg gtttattgat gatgagcata tgattgtcct caaataaaat
17161 atcaagctcg ccatactccg gaatgaccga agatgcttca ctttcctgaa gatcaatgaa
17221 cacgcggtct cccttttta caatcatatt gtttaagacg gattcgtgat tgacctttat
17281 ctgttgatgg gacatccagt cttgtatcac tggtttagaa gctttgagcg ctgttttgag
17341 tacggaaaac agccattggc cgtcctgttt ttcattgatg aggatctcaa gccctctgcc
17401 ttttggttc atgttaaatg gctcctttc gaagcggaag gctgctgttt ctcataggaa
17461 acacttacct tagctttcgc gttttttct gtgctattct tgagtaagac ttaggatatt
17521 cgatggcaag aaaggtgatt gacgtgagaa ttgtgaacgc agcaactgca gaacaggaga
17581 gctttatcaa ggagctgtct atggagctga tccatgatgt atttcctctt tatttctccg
17641 aactggacat tcagcgcttg aaaaagaaag gcgttctgtc tttaaataac cattattacc
17701 aaggaacatt aaaagaagca tttcaaatta tggcttgtct gcaaatgata catattatcc
17761 tgaccaagcc ttcgccgcac tctgatttga gtgatcaggc gattttgaa aaaaacagca
17821 agatgctgaa tgattttggg atttatttc cgtttgcttt ttctgacttt caaaagaaga
17881 ctaacaaagc ctttttcggt caaagaaggc tgatataatc atgcggcaag ggcttttcta
17941 tttttagaaa agctctttt gtatcagaga aatcatatca taaaaccttt cctctaactc
18001 ccttttaaa cggctcgtgt ctgaacatac taatgattga aggggtgct gacaatgagt
18061 tcagttaaag atacaatgac aacgcaggtg gcaaccgttt ctccgaatca aacgattcag
18121 gaagcggctt ctctaatgaa acagcataac gtcggggcga tccccgttgt agagcaaggt
18181 gttttaaaag gaatgctgac tgaccgtgac attgcattaa gaactacagc tcagggccgt
18241 gatggccaga cacccgtttc agaagtgatg tcaacagaac tcgtatcagg aaaccctaat
18301 atgagtctgg aagacgcgtc gcagctgatg gcccagcacc aaatccgccg ccttcctatt
18361 gtagatcaaa acaatctagt cgggatcgtt gcgcttggag acctggcagt caatcagatg
18421 tcgaacgagt ctgcgggatc agcgctgaca aacatttctc accaaaacat tcattaataa
18481 gaaagagctt gcagtgtgca ggctctttct tcacataaaa ccttacttt tgaaagcaga
18541 cttgtttcgg ggtatagtga gtgtatacat atgtctcaat tcgtactaaa ggagttgtac
18601 ccagtgatta aagcgttaat ttttgatttt gacgggctta ttctagatac agaaacacac
18661 gaatatgagg ttcttcagga aatatttgaa gagcacggct cagtgctgcc gctatctgtc
18721 tggggaaagg tcatcggaac tgctgcgggt ttccggcctt ttgaatattt agaagagcag
18781 atcgggaaaa agctgaacca tgaagagctc acacaattga gaagagcg gtttgccaaa
18841 cgcatggaat cagaaaaagc gagacctggt gtcgaagcgt atttgaatgc ggcaaaggat
18901 ttaggcttaa aaataggcct tgcctccagc tctgattata aatgggtgtc cggccatttg
18961 aagcaaatcg gcctgtttga tgattttgaa gttattcaaa cggcggatga tgtggaagag
19021 gtgaagccga atcctgaact ctatttattg gcggcaaaga acctgggggt atcgccagcg
19081 gaatgtctcg cgtttgagga ttctgtcaat ggttcgattg ctgcgaaacg tgcaggcatg
19141 aagtgtgtca ttgtcccgaa taaagtaacg ggtaccttga tgtttgaaga ctatgatcac
19201 aggcttgaat caatggcgga gatggagctc gccctattgc ttgatcatct gaactcacaa
19261 aactagaaag gagcgagtag gttgtctgag aaattagatt tgacccggtt tgaaaagaaa
19321 atggttatcc gcaatatcga agagaaagac atcgacaaga ttatcgatct tcaaaaggac
19381 tgctttccag gaatggagcc ttggaagcgg gagcatttaa tcagccattt ggagcatttt
19441 ccggaaggac agttttgtgc agaattcgaa ggtgaaatta tcggttcgtg ctcaagtctc
19501 ctgattaact ttgatgaata tgatgaccgc catacgtggc aggacattac agatgacggt
19561 tatatcacca accataatcc tgacggcttg aatatgtacg gaattgaagt catggtgcac
19621 ccgaaataca gacgaatgaa gatcggccac cgtttgtacg aggcgagaaa ggacttagcc
19681 agacgcttaa gcctgaaaag catcatcata ggcggacgga ttccaaacta tcacaaatat
19741 gcagaggaaa tgacagcgag agagtatgtt gaacaggtga cacgccacca aatttacgat
19801 ccggttcttt cttttcagct gatgaacggc tttaccctta tgcgaattaa cccgaactat
19861 ctcccggatg atacagcttc gatcaagtat gcgacgctga tggaatggaa taatgtcgat
19921 tatctaccgc agcagacaaa acgctattat aaatcggcgt tccctgttag aatttgtgtg
19981 atccaatacg aaatgaagaa aatttattcc tttgaggaat ttgcgaatca agtagaatac
20041 tatgtcgatg ttgcttccga cgcaagatct gattttgcgg tgttcccgga aattttcaca
20101 acccagctga tgtccttcct tgaggaacgg tcaccgagct ggcggtgca gagaattacc
20161 gagtatacag aagattacat cagcctgttt actgacttgg ctgtgaagta taacgtcaac
20221 attatcggcg gatctcattt cgtcgaagag gaaggcaaga tctataatat cgcttacctg
20281 ttcagacggg acggaacgat cgagaagcaa tacaaactcc atattacgcc gaatgaacgc
20341 aaatggtggg ggatcagcgc aggagaccaa gttcgcgtgt ttgatacgga ctgcgggaaa
```

```
20401 atcgcgatcc agatctgtta tgacattgaa tttcctgagc ttgcccggat tgcggctgat
20461 aaaggagcca aaatcatctt tacgccattt tgtacagaag accgtcaagg ctatctgcgt
20521 gtcagatact gttcgcaggc tagagcggtt gaaaatcaaa tttatacggt tatctctgga
20581 acggtcggaa accttccgca aacggaaaac atggatatcc aatacgccca gtcaggcatc
20641 tttgccccgt ctgattttga attcgcccga gacggcattg tcggcgaaac aaacccgaat
20701 attgaaatgg tcgtcatcgg cgatgttgac ctggaaattc tcagaagaca gcgccaaaac
20761 ggtacagtgc gccagctaaa agacagacga cgtgatattt atcatattca atataaaaaa
20821 taattcccaa aaaacccgcc tgaattggcg gttttttta acaaaagcgg aattgtttag
20881 gtgctttctt taaaataaaa gtaaattgta tagtggatgt gccttatgga gtttctgtat
20941 tttcgccatt tcctatatca tacagaaaac ggctaggctt cacattgcta ttgcaatggc
21001 tgtccaagtt gtttcgagtg cgacctttat cagtacgatg ctgagcattg tcactttgcc
21061 tgttttgctt tggaagctgc atcctctttc ttcttgagaa aggggatgtt ttattattta
21121 cgcggtttat tgactctgac ccggtctggc tttatattga aggcagggaa atcatcacca
21181 agacatcaca taaagagaag gtctgtttca attgaattgg cattataggg aacgctaatg
21241 aaatggagat gatggggatg gaaaacattc agcaaaatca gggattaaag caaaaagatg
21301 agcaatttgt gtggcatgcc atgaagggag cgcatcaagc ggacagcctg atagcccaga
21361 aggccgaagg ggcctgggta accgacacag acggacgccg ctatttggat gcgatgtccg
21421 gtttgtggtg cgtcaacatt ggttacggca gaaaggagct tgcggaggct gcctatgagc
21481 aactaaagga gctgccttac tacccgttaa cgcaaagtca cgcacccgca attcaactgg
21541 cggaaaagct gaatgaatgg cttggcggcg attatgttat tttttttcc aacagcggat
21601 cggaagcaaa cgaaactgct tttaaaattg cccgccagta ccatctgcaa aacggcgacc
21661 acagccgtta taaattcatc tcaagatatc gggcatacca cggcaataca ttgggagcgc
21721 tctcagctac cggacaggcg cagcggaaat ataaatacga gcctttgagc caagggttcc
21781 tgcatgcagc tccgccagat atataccg
```

//

Nov 8 2004 13:44:10